

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 09/881,736A  
Source: IFW16  
Date Processed by STIC: 12/20/04

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IFW16

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/881,736A

DATE: 12/20/2004

TIME: 12:22:01

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Output Set: N:\CRF4\12202004\I881736A.raw

4 <110> APPLICANT: Glotzer, Michael  
 5 Jantsch-Plunger, Verena  
 6 Romano, Alper  
 7 Mishima, Masanori  
 8 Kaitna, Susanne  
 10 <120> TITLE OF INVENTION: Cyk-4 polypeptides, DNA molecules encoding them and their  
 use in screening  
 11 methods  
 13 <130> FILE REFERENCE: 0652.2260001/EKS/AES  
 15 <140> CURRENT APPLICATION NUMBER: US 09/881,736A  
 16 <141> CURRENT FILING DATE: 2001-06-18  
 18 <150> PRIOR APPLICATION NUMBER: EP 00 112 880.0  
 19 <151> PRIOR FILING DATE: 2000-06-19  
 21 <150> PRIOR APPLICATION NUMBER: EP 01 110 554.1  
 22 <151> PRIOR FILING DATE: 2001-04-30  
 24 <150> PRIOR APPLICATION NUMBER: 60/241,231  
 25 <151> PRIOR FILING DATE: 2000-10-18  
 27 <150> PRIOR APPLICATION NUMBER: To be determined  
 28 <151> PRIOR FILING DATE: 2001-06-13  
 31 <160> NUMBER OF SEQ ID NOS: 8  
 33 <170> SOFTWARE: PatentIn Ver. 2.1  
 37 <210> SEQ ID NO: 1  
 38 <211> LENGTH: 3050  
 39 <212> TYPE: DNA  
 40 <213> ORGANISM: Homo sapiens  
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 43 <221> NAME/KEY: 5'UTR  
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 46 <220> FEATURE:  
 47 <221> NAME/KEY: CDS  
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 58 cgtgtgaaag atg gat act atg atg ctg aat gtg cgg aat ctg ttt gag 109  
 59 Met Asp Thr Met Met Leu Asn Val Arg Asn Leu Phe Glu  
 60 1 5 10  
 62 cag ctt gtg cgc cgg gtg gag att ctc agt gaa gga aat gaa gtc caa 157  
 63 Gln Leu Val Arg Arg Val Glu Ile Leu Ser Glu Gly Asn Glu Val Gln  
 64 15 20 25  
 66 ttt atc cag ttg gcg aag gac ttt gag gat ttc cgt aaa aag tgg cag 205  
 67 Phe Ile Gln Leu Ala Lys Asp Phe Glu Asp Phe Arg Lys Lys Trp Gln

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70	agg act gac cat gag ctg ggg aaa tac aag gat ctt ttg atg aaa gca				253
71	Arg Thr Asp His Glu Leu Gly Lys Tyr Lys Asp Leu Leu Met Lys Ala				
72	50	55	60		
74	gag act gag cga agt gct ctg gat gtt aag ctg aag cat gca cgt aat				301
75	Glu Thr Glu Arg Ser Ala Leu Asp Val Lys Leu Lys His Ala Arg Asn				
76	65	70	75		
78	cag gtg gat gta gag atc aaa cgg aga cag aga gct gag gct gac tgc				349
79	Gln Val Asp Val Glu Ile Lys Arg Arg Gln Arg Ala Glu Ala Asp Cys				
80	80	85	90		
82	gaa aag ctg gaa cga cag att cag ctg att cga gag atg ctc atg tgt				397
83	Glu Lys Leu Glu Arg Gln Ile Gln Leu Ile Arg Glu Met Leu Met Cys				
84	95	100	105		
86	gac aca tct ggc agc att caa cta agc gag gag caa aaa tca gct ctg				445
87	Asp Thr Ser Gly Ser Ile Gln Leu Ser Glu Glu Gln Lys Ser Ala Leu				
88	110	115	120	125	
90	gct ttt ctc aac aga ggc caa cca tcc agc agc aat gct ggg aac aaa				493
91	Ala Phe Leu Asn Arg Gly Gln Pro Ser Ser Ser Asn Ala Gly Asn Lys				
92	130	135	140		
94	aga cta tca acc att gat gaa tct ggt tcc att tta tca gat atc agc				541
95	Arg Leu Ser Thr Ile Asp Glu Ser Gly Ser Ile Leu Ser Asp Ile Ser				
96	145	150	155		
98	ttt gac aag act gat gaa tca ctg gat tgg gac tct tct ttg gtg aag				589
99	Phe Asp Lys Thr Asp Glu Ser Leu Asp Trp Asp Ser Ser Leu Val Lys				
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102	act ttc aaa ctg aag aag aga gaa aag agg cgc tct act agc cga cag				637
103	Thr Phe Lys Leu Lys Lys Arg Glu Lys Arg Arg Ser Thr Ser Arg Gln				
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106	ttt gtt gat ggt ccc cct gga cct gta aag aaa act cgt tcc att ggc				685
107	Phe Val Asp Gly Pro Pro Gly Pro Val Lys Lys Thr Arg Ser Ile Gly				
108	190	195	200	205	
110	tct gca gta gac cag ggg aat gaa tcc ata gtt gca aaa act aca gtg				733
111	Ser Ala Val Asp Gln Gly Asn Glu Ser Ile Val Ala Lys Thr Thr Val				
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114	act gtt ccc aat gat ggc ggg ccc atc gaa gct gtg tcc act att gag				781
115	Thr Val Pro Asn Asp Gly Gly Pro Ile Glu Ala Val Ser Thr Ile Glu				
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118	act gtg cca tat tgg acc agg agc cga agg aaa aca ggt act tta caa				829
119	Thr Val Pro Tyr Trp Thr Arg Ser Arg Arg Lys Thr Gly Thr Leu Gln				
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122	cct tgg aac agt gac tcc acc ctg aac agc agg cag ctg gag cca aga				877
123	Pro Trp Asn Ser Asp Ser Thr Leu Asn Ser Arg Gln Leu Glu Pro Arg				
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131	Leu His Asp Phe Val Ser Lys Thr Val Ile Lys Pro Glu Ser Cys Val				
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134 cca tgt gga aag cgg ata aaa ttt ggc aaa tta tct ctg aag tgt cga	1021
135 Pro Cys Gly Lys Arg Ile Lys Phe Gly Lys Leu Ser Leu Lys Cys Arg	
136 305 310 315	
138 gac tgt cgt gtg gtc tct cat cca gaa tgt cgg gac cgc tgt ccc ctt	1069
139 Asp Cys Arg Val Val Ser His Pro Glu Cys Arg Asp Arg Cys Pro Leu	
140 320 325 330	
142 ccc tgc att cct acc ctg ata gga aca cct gtc aag att gga gag gga	1117
143 Pro Cys Ile Pro Thr Leu Ile Gly Thr Pro Val Lys Ile Gly Glu Gly	
144 335 340 345	
146 atg ctg gca gac ttt gtg tcc cag act tct cca atg atc ccc tcc att	1165
147 Met Leu Ala Asp Phe Val Ser Gln Thr Ser Pro Met Ile Pro Ser Ile	
148 350 355 360 365	
150 gtt gtg cat tgt gta aat gag att gag caa aga ggt ctg act gag aca	1213
151 Val Val His Cys Val Asn Glu Ile Glu Gln Arg Gly Leu Thr Glu Thr	
152 370 375 380	
154 ggc ctg tat agg atc tct ggc tgt gac cgc aca gta aaa gag ctg aaa	1261
155 Gly Leu Tyr Arg Ile Ser Gly Cys Asp Arg Thr Val Lys Glu Leu Lys	
156 385 390 395	
158 gag aaa ttc ctc aga gtg aaa act gta ccc ctc ctc agc aaa gtg gat	1309
159 Glu Lys Phe Leu Arg Val Lys Thr Val Pro Leu Leu Ser Lys Val Asp	
160 400 405 410	
162 gat atc cat gct atc tgt agc ctt cta aaa gac ttt ctt cga aac ctc	1357
163 Asp Ile His Ala Ile Cys Ser Leu Leu Lys Asp Phe Leu Arg Asn Leu	
164 415 420 425	
166 aaa gaa cct ctt ctg acc ttt cgc ctt aac aga gcc ttt atg gaa gca	1405
167 Lys Glu Pro Leu Leu Thr Phe Arg Leu Asn Arg Ala Phe Met Glu Ala	
168 430 435 440 445	
170 gca gaa atc aca gat gaa gac aac agc ata gct gcc atg tac caa gct	1453
171 Ala Glu Ile Thr Asp Glu Asp Asn Ser Ile Ala Ala Met Tyr Gln Ala	
172 450 455 460	
174 gtt ggt gaa ctg ccc cag gcc aac agg gac aca tta gct ttc ctc atg	1501
175 Val Gly Glu Leu Pro Gln Ala Asn Arg Asp Thr Leu Ala Phe Leu Met	
176 465 470 475	
178 att cac ttg cag aga gtg gct cag agt cca cat act aaa atg gat gtt	1549
179 Ile His Leu Gln Arg Val Ala Gln Ser Pro His Thr Lys Met Asp Val	
180 480 485 490	
182 gcc aat ctg gct aaa gtc ttt ggc cct aca ata gtg gcc cat gct gtg	1597
183 Ala Asn Leu Ala Lys Val Phe Gly Pro Thr Ile Val Ala His Ala Val	
184 495 500 505	
186 ccc aat cca gac cca gtg aca atg tca cag gac atc aag cgt caa ccc	1645
187 Pro Asn Pro Asp Pro Val Thr Met Ser Gln Asp Ile Lys Arg Gln Pro	
188 510 515 520 525	
190 aag gtg gtt gag cgc ctg ctt tcc ttg cct ctg gag tat tgg agt cag	1693
191 Lys Val Val Glu Arg Leu Leu Ser Leu Pro Leu Glu Tyr Trp Ser Gln	
192 530 535 540	
194 ttc atg atg gtg gag caa gag aac att gac ccc cta cat gtc att gaa	1741
195 Phe Met Met Val Glu Gln Glu Asn Ile Asp Pro Leu His Val Ile Glu	
196 545 550 555	
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203 Leu Leu Gly Pro Val Thr Thr Pro Glu His Gln Leu Leu Lys Thr Pro  
204 575 580 585  
206 tca tct agt tcc ctg tca cag aga gtc cgt tcc acc ctc acc aag aac 1885  
207 Ser Ser Ser Leu Ser Gln Arg Val Arg Ser Thr Leu Thr Lys Asn  
208 590 595 600 605  
210 act cct aga ttt ggg agc aaa agc aag tct gcc act aac cta gga cga 1933  
211 Thr Pro Arg Phe Gly Ser Lys Ser Lys Ala Thr Asn Leu Gly Arg  
212 610 615 620  
214 caa ggc aac ttt ttt gct tct cca atg ctc aag tga agtcacatct 1979  
215 Gln Gly Asn Phe Phe Ala Ser Pro Met Leu Lys  
216 625 630  
218 gcctgttaact tcccaggcatt gactgactat aagaaaaggac acatctgtac tctgctctgc 2039  
220 agcctccctgt actcattact acttttagca ttctccaggc ttttactcaa gtttaattgt 2099  
222 gcatgaggggt tttattaaaa ctatataatat ctcccccttcc ttctcctcaa gtcacataat 2159  
224 atcagcactt tgtgtggtc attgttggga gcttttagat gagacatctt tccaggggta 2219  
226 gaagggttag tatgaattt gttgtgattc tttttggga agggggttat tgttcccttg 2279  
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242 aaaattgtat tcattctgtat gcttggcccc cataccccc accttgccta gtggagccca 2759  
244 acttctaaag gtcaatataat catcctttgg catcccaact accaataaaag agtaggctat 2819  
246 aagggaaagat tgtcaatatt ttgtggtaag aaaagctaca gtcattttt cttgcactt 2879  
248 tggatgctga aattttccc atgaaacata gccacatcta gatagatgtg agcttttct 2939  
250 tctgttaaaa ttattcttaa tggtaaaa aacgatttc ttctgtagaa tggactt 2999  
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259 <213> ORGANISM: Homo sapiens  
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267 20 25 30  
269 Leu Ala Lys Asp Phe Glu Asp Phe Arg Lys Lys Trp Gln Arg Thr Asp  
270 35 40 45  
272 His Glu Leu Gly Lys Tyr Lys Asp Leu Leu Met Lys Ala Glu Thr Glu  
273 50 55 60  
275 Arg Ser Ala Leu Asp Val Lys Leu Lys His Ala Arg Asn Gln Val Asp  
276 65 70 75 80  
278 Val Glu Ile Lys Arg Arg Gln Arg Ala Glu Ala Asp Cys Glu Lys Leu  
279 85 90 95

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288 130 135 140  
290 Thr Ile Asp Glu Ser Gly Ser Ile Leu Ser Asp Ile Ser Phe Asp Lys  
291 145 150 155 160  
293 Thr Asp Glu Ser Leu Asp Trp Asp Ser Ser Leu Val Lys Thr Phe Lys  
294 165 170 175  
296 Leu Lys Lys Arg Glu Lys Arg Arg Ser Thr Ser Arg Gln Phe Val Asp  
297 180 185 190  
299 Gly Pro Pro Gly Pro Val Lys Lys Thr Arg Ser Ile Gly Ser Ala Val  
300 195 200 205  
302 Asp Gln Gly Asn Glu Ser Ile Val Ala Lys Thr Thr Val Thr Val Pro  
303 210 215 220  
305 Asn Asp Gly Gly Pro Ile Glu Ala Val Ser Thr Ile Glu Thr Val Pro  
306 225 230 235 240  
308 Tyr Trp Thr Arg Ser Arg Arg Lys Thr Gly Thr Leu Gln Pro Trp Asn  
309 245 250 255  
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312 260 265 270  
314 Asp Ser Val Gly Thr Pro Gln Ser Asn Gly Gly Met Arg Leu His Asp  
315 275 280 285  
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320 Lys Arg Ile Lys Phe Gly Lys Leu Ser Leu Lys Cys Arg Asp Cys Arg  
321 305 310 315 320  
323 Val Val Ser His Pro Glu Cys Arg Asp Arg Cys Pro Leu Pro Cys Ile  
324 325 330 335  
326 Pro Thr Leu Ile Gly Thr Pro Val Lys Ile Gly Glu Gly Met Leu Ala  
327 340 345 350  
329 Asp Phe Val Ser Gln Thr Ser Pro Met Ile Pro Ser Ile Val Val His  
330 355 360 365  
332 Cys Val Asn Glu Ile Glu Gln Arg Gly Leu Thr Glu Thr Gly Leu Tyr  
333 370 375 380  
335 Arg Ile Ser Gly Cys Asp Arg Thr Val Lys Glu Leu Lys Glu Lys Phe  
336 385 390 395 400  
338 Leu Arg Val Lys Thr Val Pro Leu Leu Ser Lys Val Asp Asp Ile His  
339 405 410 415  
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342 420 425 430  
344 Leu Leu Thr Phe Arg Leu Asn Arg Ala Phe Met Glu Ala Ala Glu Ile  
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Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 10

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